

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: SOPPET, DANIEL R.
RUBEN, STEVEN M.
- (ii) TITLE OF INVENTION: CARDIAC AND PANCREATIC PROTEIN AND GENE
- (iii) NUMBER OF SEQUENCES: 42
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
 - (B) STREET: 1100 NEW YORK AVENUE, SUITE 600
 - (C) CITY: WASHINGTON
 - (D) STATE: DC
 - (E) COUNTRY: US
 - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: To be assigned
 - (B) FILING DATE: Herewith
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 60/042,855
 - (B) FILING DATE: 28-MAR-1997
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: STEFFE, ERIC K.
 - (B) REGISTRATION NUMBER: 36,688
 - (C) REFERENCE/DOCKET NUMBER: 1488.0620001
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (202) 371-2600
 - (B) TELEFAX: (202) 371-2540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2745 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 233..1423
- (ix) FEATURE:
 - (A) NAME/KEY: sig_peptide

(B) LOCATION: 233..328

(ix) FEATURE:

(A) NAME/KEY: mat_peptide
(B) LOCATION: 329..1423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GCAGCGGCAC	GGCAGCAGCG	GCAACAAGTG	CCGGACTAGC	AGAGCCAAGC	CGGAGCAGTC	60										
CCTGCCGCCG	ACACCGCCGG	GCCGCCCGTC	CGGGGCCCG	CGCATGGAGC	GTGAGCTGCG	120										
GCGGTCGCCG	GGGCTGAGCC	GCGCGGAGCG	CCGGGACGTG	GATGTGGCCG	CGATCTCCCG	180										
CCCTTGCCCC	CGCCCCGCCG	AGCTGGAGCT	GCTCCCGGAC	AAGATATGAG	AA ATG	235										
				Met												
				-32												
AGT	GTT	GGA	CGT	CGA	AGA	ATA	AAG	TTG	TTG	GGT	ATC	CTG	ATG	ATG	GCA	283
Ser	Val	Gly	Arg	Arg	Arg	Ile	Lys	Leu	Leu	Gly	Ile	Leu	Met	Met	Ala	
-30						-25					-20					
AAT	GTC	TTC	ATT	TAT	TTT	ATT	ATG	GAA	GTC	TCC	AAA	AGC	AGT	AGC	CAA	331
Asn	Val	Phe	Ile	Tyr	Phe	Ile	Met	Glu	Val	Ser	Lys	Ser	Ser	Ser	Gln	
-15						-10					-5				1	
GAA	AAA	AAT	GGA	AAA	GGG	GAA	GTA	ATA	ATA	CCC	AAA	GAG	AAG	TTC	TGG	379
Glu	Lys	Asn	Gly	Lys	Gly	Glu	Val	Ile	Ile	Pro	Lys	Glu	Lys	Phe	Trp	
5						10					15					
AAG	ATA	TCT	ACC	CCT	CCC	GAG	GCA	TAC	TGG	AAC	CGA	GAG	CAA	GAG	AAG	427
Lys	Ile	Ser	Thr	Pro	Pro	Glu	Ala	Tyr	Trp	Asn	Arg	Glu	Gln	Glu	Lys	
20						25					30					
CTG	AAC	CGG	CAG	TAC	AAC	CCC	ATC	CTG	AGC	ATG	CTG	ACC	AAC	CAG	ACG	475
Leu	Asn	Arg	Gln	Tyr	Asn	Pro	Ile	Leu	Ser	Met	Leu	Thr	Asn	Gln	Thr	
35						40					45					
GGG	GAG	GCG	GGC	AGG	CTC	TCC	AAT	ATA	AGC	CAT	CTG	AAC	TAC	TGC	GAA	523
Gly	Glu	Ala	Gly	Arg	Leu	Ser	Asn	Ile	Ser	His	Leu	Asn	Tyr	Cys	Glu	
50						55					60					65
CCT	GAC	CTG	AGG	GTC	ACG	TCG	GTG	GTT	ACG	GGT	TTT	AAC	AAC	TTG	CCG	571
Pro	Asp	Leu	Arg	Val	Thr	Ser	Val	Val	Thr	Gly	Phe	Asn	Asn	Leu	Pro	
70						75					80					
GAC	AGA	TTT	AAA	GAC	TTT	CTG	CTG	TAT	TTG	AGA	TGC	CGC	AAT	TAT	TCA	619
Asp	Arg	Phe	Asp	Phe	Leu	Leu	Tyr	Leu	Arg	Cys	Arg	Asn	Tyr	Ser		
85						90					95					
CTG	CTT	ATA	GAT	CAG	CCG	GAT	AAG	TGT	GCA	AAG	AAA	CCT	TTC	TTG	TTG	667
Leu	Leu	Ile	Asp	Gln	Pro	Asp	Lys	Cys	Ala	Lys	Lys	Pro	Phe	Leu	Leu	
100						105					110					
CTG	GCG	ATT	AAG	TCC	CTC	ACT	CCA	CAT	TTT	GCC	AGA	AGG	CAA	GCA	ATC	715
Leu	Ala	Ile	Lys	Ser	Leu	Thr	Pro	His	Phe	Ala	Arg	Arg	Gln	Ala	Ile	
115						120					125					
CGG	GAA	TCC	TGG	GGC	CAA	GAA	AGC	AAC	GCA	GGG	AAC	CAA	ACG	GTG	GTG	763
Arg	Glu	Ser	Trp	Gly	Gln	Glu	Ser	Asn	Ala	Gly	Asn	Gln	Thr	Val	Val	
130						135					140					145

CGA GTC TTC CTG CTG GGC CAG ACA CCC CCA GAG GAC AAC CAC CCC GAC Arg Val Phe Leu Leu Gly Gln Thr Pro Pro Glu Asp Asn His Pro Asp 150 155 160	811
CTT TCA GAT ATG CTG AAA TTT GAG AGT GAG AAG CAC CAA GAC ATT CTT Leu Ser Asp Met Leu Lys Phe Glu Ser Glu Lys His Gln Asp Ile Leu 165 170 175	859
ATG TGG AAC TAC AGA GAC ACT TTC TTC AAC TTG TCT CTG AAG GAA GTG Met Trp Asn Tyr Arg Asp Thr Phe Phe Asn Leu Ser Leu Lys Glu Val 180 185 190	907
CTG TTT CTC AGG TGG GTA AGT ACT TCC TGC CCA GAC ACT GAG TTT GTT Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Thr Glu Phe Val 195 200 205	955
TTC AAG GCC GAT GAC GAT GTT TTT GTG AAC ACC CAT CAC ATC CTG AAT Phe Lys Gly Asp Asp Asp Val Phe Val Asn Thr His His Ile Leu Asn 210 215 220 225	1003
TAC TTG AAT AGT TTA TCC AAG ACC AAA GCC AAA GAT CTC TTC ATA GGT Tyr Leu Asn Ser Leu Ser Lys Thr Lys Ala Lys Asp Leu Phe Ile Gly 230 235 240	1051
GAT GTG ATC CAC AAT GCT GGA CCT CAT CGG GAT AAG AAG CTG AAG TAC Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu Lys Tyr 245 250 255	1099
TAC ATC CCA GAA GTT GTT TAC TCT GGC CTC TAC CCA CCC TAT GCA GGG Tyr Ile Pro Glu Val Val Tyr Ser Gly Leu Tyr Pro Pro Tyr Ala Gly 260 265 270	1147
GGA GGG GGG TTC CTC TAC TCC GGC CAC CTG GCC CTG AGG CTG TAC CAT Gly Gly Gly Phe Leu Tyr Ser Gly His Leu Ala Leu Arg Leu Tyr His 275 280 285	1195
ATC ACT GAC CAG GTC CAT CTC TAC CCC ATT GAT GAC GTT TAT ACT GGA Ile Thr Asp Gln Val His Leu Tyr Pro Ile Asp Asp Val Tyr Thr Gly 290 295 300 305	1243
ATG TGC CTT CAG AAA CTC GGC CTC GTT CCA GAG AAA CAC AAA GGC TTC Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His Lys Gly Phe 310 315 320	1291
AGG ACA TTT GAT ATC GAG GAG AAA AAC AAA AAT AAC ATC TGC TCC TAT Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Asn Asn Ile Cys Ser Tyr 325 330 335	1339
GTA GAT CTG ATG TTA GTA CAT AGT AGA AAA CCT CAA GAG ATG ATT GAT Val Asp Leu Met Leu Val His Ser Arg Lys Pro Gln Glu Met Ile Asp 340 345 350	1387
ATT TGG TCT CAG TTG CAG AGT GCT CAT TTA AAA TGC TAAAATAGAT Ile Trp Ser Gln Leu Gln Ser Ala His Leu Lys Cys 355 360 365	1433
ACAAACTCAA TTTGCATAG AAAGGTGTAT TTTGAATAGT TCCCATGTTG TGTTCTCACA	1493
TTAGAGTAAT TTCTATATTA AACCATGAAA ATTGCCTTTA TGAGTGATAC CCATTGAGG	1553
GCCTCTAAAC CCTTCAATTG GGTACTCACG TGAAGAGGGA AAGCGGAAGA TGGTAATT	1613

TTTTTATGGA TGATATGGCA GGATGATTGG TTCTGATCTT ACCGGCTAGT GGTCATT	1673
AAAAAAACTTG TACCCCTCTTA TCTGAAATCC TGTTTCTGGA ATTTGGCCAT TTTAAGTGAT	1733
TTTGTTCGCC CTCTTCTATA ATATTCTAC TTCCCATAAT AATGACTGAT TTATTTGTAA	1793
TTCAGGTATT TATAAACCTA TTGGCTACAA AGACTTTGTT AAACATTATC CAGTGGTTT	1853
CGTGAAATGG AATTATGTTT ATTTTATGG GATTTGGGT AATTTAAAT TGTCTAGAAA	1913
ACTGAAATTT CAGTTGTCAG TTGTGGAATT CAGTTTTCA ATTGTGGAAA TTTCCTGCCA	1973
CCCCAACAGT ATTTTGTGT GTTAATTAAT TTTGCAAAAT GAGAACATG GTGTGACACT	2033
CATCTAATTT ATCTTGTGT GATGTTATGG TCATAATAAG GAGAAAGAGG GTTTAATT	2093
TCTTGTATTG GGTTTCTGG TGGTATCATA GTGTAATTAGT AGTATTGAA AATCAGTGTG	2153
ATTCCTTAAT GGCCAACTGA AGATTGAATT GCCGCTAACCA ACCATATCGT GTTAGTGAAT	2213
TTTCAATATG GACCAGGAAG GCATATGTAT TTTGAACTTG AGTGAAGAGG TTGAAGTTAC	2273
AGACTTTGC ATAGATGGTT TGTCAATTAA AAATTCCAGA ATTTATTATT GCCATATT	2333
CACATGCTGC TTATACAAGA TTATTATTGA GTAGTAACTG TTCCCTGTCT ATGTAGAAGT	2393
GCCTGTGTTT TTATTATTG TTCCAGATCA AAGACCAAAA CATTCTTA AATATCTCTT	2453
ATGTAATATT TTATTGTAT ACAGTGTGT TGATGAAATA TTTAACTAGA GCATGATATT	2513
TTAAATGTTA AGGTGTAACA TATGTTAAAT AAAACTGTTA TTTTGAAATT TTAAAATTG	2573
TTTTTGGGG GTATGAACTA CTAGAGTTA AAATTCTGCC AACTATTAC TTATATGTAC	2633
TATTGTGTAA CATACTTCT TGAAATATT TTGTTATAG AATTGAAGGT TCTTATCAGA	2693
TGGGATACTG GGGATTATAA ACAATGGAAA TAAAGCCACT GTATTTTAA AA	2745

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 397 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Ser Val Gly Arg Arg Arg Ile Lys Leu Leu Gly Ile Leu Met Met
-32 -30 -25 -20

Ala Asn Val Phe Ile Tyr Phe Ile Met Glu Val Ser Lys Ser Ser Ser
-15 -10 -5

Gln Glu Lys Asn Gly Lys Gly Glu Val Ile Ile Pro Lys Glu Lys Phe
1 5 10 15

Trp Lys Ile Ser Thr Pro Pro Glu Ala Tyr Trp Asn Arg Glu Gln Glu
20 25 30

Lys Leu Asn Arg Gln Tyr Asn Pro Ile Leu Ser Met Leu Thr Asn Gln
35 40 45

Thr Gly Glu Ala Gly Arg Leu Ser Asn Ile Ser His Leu Asn Tyr Cys
50 55 60

Glu Pro Asp Leu Arg Val Thr Ser Val Val Thr Gly Phe Asn Asn Leu
65 70 75 80

Pro Asp Arg Phe Lys Asp Phe Leu Leu Tyr Leu Arg Cys Arg Asn Tyr
85 90 95

Ser Leu Leu Ile Asp Gln Pro Asp Lys Cys Ala Lys Lys Pro Phe Leu
100 105 110

Leu Leu Ala Ile Lys Ser Leu Thr Pro His Phe Ala Arg Arg Gln Ala
115 120 125

Ile Arg Glu Ser Trp Gly Gln Glu Ser Asn Ala Gly Asn Gln Thr Val
130 135 140

Val Arg Val Phe Leu Leu Gly Gln Thr Pro Pro Glu Asp Asn His Pro
145 150 155 160

Asp Leu Ser Asp Met Leu Lys Phe Glu Ser Glu Lys His Gln Asp Ile
165 170 175

Leu Met Trp Asn Tyr Arg Asp Thr Phe Phe Asn Leu Ser Leu Lys Glu
180 185 190

Val Leu Phe Leu Arg Trp Val Ser Thr Ser Cys Pro Asp Thr Glu Phe
195 200 205

Val Phe Lys Gly Asp Asp Val Phe Val Asn Thr His His Ile Leu
210 215 220

Asn Tyr Leu Asn Ser Leu Ser Lys Thr Lys Ala Lys Asp Leu Phe Ile
225 230 235 240

Gly Asp Val Ile His Asn Ala Gly Pro His Arg Asp Lys Lys Leu Lys
245 250 255

Tyr Tyr Ile Pro Glu Val Val Tyr Ser Gly Leu Tyr Pro Pro Tyr Ala
260 265 270

Gly Gly Gly Phe Leu Tyr Ser Gly His Leu Ala Leu Arg Leu Tyr
275 280 285

His Ile Thr Asp Gln Val His Leu Tyr Pro Ile Asp Asp Val Tyr Thr
290 295 300

Gly Met Cys Leu Gln Lys Leu Gly Leu Val Pro Glu Lys His Lys Gly
305 310 315 320

Phe Arg Thr Phe Asp Ile Glu Glu Lys Asn Lys Asn Asn Ile Cys Ser
325 330 335

Tyr Val Asp Leu Met Leu Val His Ser Arg Lys Pro Gln Glu Met Ile
340 345 350

Asp Ile Trp Ser Gln Leu Gln Ser Ala His Leu Lys Cys
355 360 365

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not relevant
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Gln	Ser	Lys	His	Arg	Lys	Leu	Leu	Leu	Arg	Cys	Leu	Leu	Val	Leu	Pro
1					5				10					15	
Leu	Ile	Leu	Leu	Val	Asp	Tyr	Cys	Gly	Leu	Leu	Thr	His	Leu	His	Glu
					20			25					30		
Leu	Asn	Phe	Glu	Arg	His	Phe	His	Tyr	Pro	Leu	Asn	Asp	Asp	Thr	Gly
					35			40				45			
Ser	Gly	Ser	Ala	Ser	Ser	Gly	Leu	Asp	Lys	Phe	Ala	Tyr	Leu	Arg	Val
					50			55			60				
Pro	Ser	Phe	Thr	Ala	Glu	Val	Pro	Val	Asp	Gln	Pro	Ala	Arg	Leu	Thr
					65			70			75		80		
Met	Leu	Ile	Lys	Ser	Ala	Val	Gly	Asn	Ser	Arg	Arg	Arg	Glu	Ala	Ile
					85			90				95			
Arg	Arg	Thr	Trp	Gly	Tyr	Glu	Gly	Arg	Phe	Ser	Asp	Val	His	Leu	Arg
					100			105				110			
Arg	Val	Phe	Leu	Leu	Gly	Thr	Ala	Glu	Asp	Ser	Glu	Lys	Asp	Val	Ala
					115			120				125			
Trp	Glu	Ser	Arg	Glu	His	Gly	Asp	Ile	Leu	Gln	Ala	Asp	Phe	Thr	Asp
					130			135				140			
Ala	Tyr	Phe	Asn	Asn	Thr	Leu	Lys	Thr	Met	Leu	Gly	Met	Arg	Trp	Ala
					145			150			155		160		
Ser	Glu	Gln	Phe	Asn	Arg	Ser	Glu	Phe	Tyr	Leu	Phe	Val	Asp	Asp	Asp
					165			170				175			
Tyr	Tyr	Val	Ser	Ala	Lys	Asn	Val	Leu	Lys	Phe	Leu	Gly	Arg	Gly	Arg
					180			185				190			
Gln	Ser	His	Gln	Pro	Glu	Leu	Leu	Phe	Ala	Gly	His	Val	Phe	Gln	Thr
					195			200				205			
Ser	Pro	Leu	Arg	His	Lys	Phe	Ser	Lys	Trp	Tyr	Val	Ser	Leu	Glu	Glu
					210			215			220				
Tyr	Pro	Phe	Asp	Arg	Trp	Pro	Pro	Tyr	Val	Thr	Ala	Gly	Ala	Phe	Ile
					225			230			235		240		
Leu	Ser	Gln	Lys	Ala	Leu	Arg	Gln	Leu	Tyr	Ala	Ala	Ser	Val	His	Leu
					245			250				255			

Pro Leu Phe Arg Phe Asp Asp Val Tyr Leu Gly Ile Val Ala Leu Lys
260 265 270

Ala Gly Ile Ser Leu Gln His Cys Asp Asp Phe Arg Phe His Arg Pro
275 280 285

Ala Tyr Lys Gly Pro Asp Ser Tyr Ser Ser Val Ile Ala Ser His Glu
290 295 300

Phe Gly Asp Pro Glu Glu Met Thr Arg Val Trp Asn Glu Cys Arg Ser
305 310 315 320

Ala Asn Tyr

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 31 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AGCAGGATCC CAAGAAAAAA ATGGAAAAGG G

31

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 29 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ATTGTCTAGA TATCTATTTT AGCATTAA

29

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GGCCGGATCC GCCATCATGA GTGTTGGACG TCGAAGAAT 39

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

ATTGTCTAGA ATTTTAAGCG TAGTCTGGGA CGTCGTATGG GTAGCATTAAATGAGCAC 60
TCTG 64

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3974 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

GGTACCTAAG TGAGTAGGGC GTCCGATCGA CGGACGCCTT TTTTTGAAT TCGTAATCAT 60
GGTCATAGCT GTTTCCTGTG TGAAATTGTT ATCCGCTCAC AATTCCACAC AACATACGAG 120
CCGGAAGCAT AAAGTGTAAA GCCTGGGTG CCTAATGAGT GAGCTAACTC ACATTAATTG 180
CGTTGCGCTC ACTGCCGCT TTCCAGTCGG GAAACCTGTC GTGCCAGCTG CATTAAATGAA 240
TCGGCCAACG CGCGGGGAGA GGCGGTTTGC GTATTGGCG CTCTTCCGCT TCCTCGCTCA 300
CTGACTCGCT GCGCTCGGTC GTTCGGCTGC GGCGAGCGGT ATCAGCTCAC TCAAAGGCGG 360
TAATAACGGTT ATCCACAGAA TCAGGGATA ACGCAGGAAA GAACATGTGA GCAAAAGGCC 420
AGCAAAAGGC CAGGAACCGT AAAAAGGCCG CGTTGCTGGC GTTTTCCAT AGGCTCCGCC 480
CCCCTGACGA GCATCACAAA AATCGACGCT CAAGTCAGAG GTGGCGAAAC CCGACAGGAC 540
TATAAAAGATA CCAGGCGTTT CCCCCCTGGAA GCTCCCTCGT GCGCTCTCCT GTTCCGACCC 600
TGCCGCTTAC CGGATAACCTG TCCGCCTTTC TCCCTCGGG AAGCGTGGCG CTTTCTCATA 660
GCTCACGCTG TAGGTATCTC AGTCGGTGT AGGTCGTTCG CTCCAAGCTG GGCTGTGTGC 720

ACGAACCCCC CGTTCAGCCC GACCCTGCG CCTTATCCGG TAACTATCGT CTTGAGTCCA	780
ACCCGGTAAG ACACGACTTA TCGCCACTGG CAGCAGCCAC TGGTAACAGG ATTAGCAGAG	840
CGAGGTATGT AGGCGGTGCT ACAGAGTTCT TGAAGTGGTG GCCTAACTAC GGCTACACTA	900
GAAGAACAGT ATTTGGTATC TGCGCTCTGC TGAAGCCAGT TACCTTCGGA AAAAGAGTTG	960
GTAGCTCTTG ATCCGGAAA CAAACCACCG CTGGTAGCGG TGGTTTTTT GTTGCAAGC	1020
AGCAGATTAC GCGCAGAAAA AAAGGATCTC AAGAAGATCC TTTGATCTTT TCTACGGGT	1080
CTGACGCTCA GTGGAACGAA AACTCACGTT AAGGGATTTT GGTCACTGAGA TTATCGTCGA	1140
CAATTGCGC GCGAAGGCGA AGCGGCATGC ATTTACGTT ACACCATCGA ATGGTGCAA	1200
ACCTTCGCG GTATGGCATG ATAGCGCCCG GAAGAGAGTC AATTCAAGGT GGTGAATGTG	1260
AAACCAGTAA CGTTATACGA TGTGCGAGAG TATGCCGGTG TCTCTTATCA GACCGTTCC	1320
CGCGTGGTGA ACCAGGCCAG CCACGTTCT GCGAAAACGC GGGAAAAAGT GGAAGGGCG	1380
ATGGCGGAGC TGAATTACAT TCCCAACCAC GTGGCACAAC AACTGGCGGG CAAACAGTCG	1440
TTGCTGATTG GCGTTGCCAC CTCCAGTCTG GCCCTGCACG CGCCGTGCA AATTGTCGCG	1500
GCGATTAAT CTCGCGCCGA TCAACTGGGT GCCAGCGTGG TGGTGTGAT GGTAGAACGA	1560
AGCGGCGTCG AAGCCTGTAA AGCGGCAGTG CACAATCTTC TCGCGCAACG CGTCAGTGGG	1620
CTGATCATTAA ACTATCCGCT GGATGACCAG GATGCCATTG CTGTGGAAGC TGCCTGCACT	1680
AATGTTCCGG CGTTATTTCT TGATGTCCT GACCAGACAC CCATCAACAG TATTATTTTC	1740
TCCCATGAAG ACGGTACGCG ACTGGCGTG GAGCATCTGG TCGCATTGGG TCACCAGCAA	1800
ATCGCGCTGT TAGCGGGCCC ATTAAGTTCT GTCTCGCGC GTCTGCGTCT GGCTGGCTGG	1860
CATAAAATATC TCACTCGCAA TCAAATTCAAG CCGATAGCGG AACGGGAAGG CGACTGGAGT	1920
GCCATGTCCG GTTTCAACA AACCATGCAA ATGCTGAATG AGGGCATCGT TCCCAGTGC	1980
ATGCTGGTTG CCAACGATCA GATGGCGCTG GGCGCAATGC GCGCCATTAC CGAGTCCGGG	2040
CTGCGCGTTG GTGCGGATAT CTCGGTAGTG GGATACGACG ATACCGAAGA CAGCTCATGT	2100
TATATCCCGC CGTTAACAC CATCAAACAG GATTTCGCC TGCTGGGGCA AACCAAGCGTG	2160
GACCGCTTGC TGCAACTCTC TCAGGGCCAG GCGGTGAAGG GCAATCAGCT GTTGCCTGTC	2220
TCACTGGTGA AAAGAAAAAC CACCCCTGGCG CCCAATACGC AAACCGCCTC TCCCCGCGCG	2280
TTGGCCGATT CATTAAATGCA GCTGGCACGA CAGGTTTCCC GACTGGAAAG CGGGCAGTGA	2340
GCGCAACGCA ATTAATGTAA GTTAGCGCGA ATTGTCGACC AAAGCGGCCA TCGTGCCTCC	2400
CCACTCCTGC AGTTGGGGG CATGGATGCG CGGATAGCCG CTGCTGGTT CCTGGATGCC	2460
GACGGATTTG CACTGCCGGT AGAACTCCGC GAGGTCGTCC AGCCTCAGGC AGCAGCTGAA	2520
CCAACTCGCG AGGGGATCGA GCCCGGGGTG GGCGAAGAAC TCCAGCATGA GATCCCCGCG	2580

CTGGAGGATC ATCCAGCCGG CGTCCCGGAA AACGATTCCG AAGCCCAACC TTTCATAGAA 2640
GGCGGCGGTG GAATCGAAAT CTCGTGATGG CAGGTTGGC GTCGCTTGGT CGGTCATTTC 2700
GAACCCCAGA GTCCCGCTCA GAAGAACTCG TCAAGAAGGC GATAGAAGGC GATGCGCTGC 2760
GAATCGGGAG CGGCGATAACC GTAAAGCACG AGGAAGCGGT CAGCCCATTG GCCGCCAAGC 2820
TCTTCAGCAA TATCACGGGT AGCCAACGCT ATGTCCTGAT AGCGGTCCGC CACACCCAGC 2880
CGGCCACAGT CGATGAATCC AGAAAAGCGG CCATTTCCA CCATGATATT CGGCAAGCAG 2940
GCATCGCCAT GGGTCACGAC GAGATCCTCG CCGTCGGGCA TGCGCGCCTT GAGCCTGGCG 3000
AACAGTCGG CTGGCGCGAG CCCCTGATGC TCTTCGTCCA GATCATCCTG ATCGACAAGA 3060
CCGGCTTCCA TCCGAGTACG TGCTCGCTCG ATGCGATGTT TCGCTTGGTG GTCGAATGGG 3120
CAGGTAGCCG GATCAAGCGT ATGCAGCCGC CGCATTGCAT CAGCCATGAT GGATACTTTC 3180
TCGGCAGGAG CAAGGTGAGA TGACAGGAGA TCCTGCCCG GCACCTCGCC CAATAGCAGC 3240
CAGTCCCTTC CCGCTTCAGT GACAACGTCG AGCACAGCTG CGCAAGGAAC GCCCGTCGTG 3300
GCCAGCCACG ATAGCCCGC TGCCCTCGTCC TGCAGTTCAT TCAGGGCACC GGACAGGTCG 3360
GTCTTGACAA AAAGAACCGG GCGCCCTGC GCTGACAGCC GGAACACGGC GGCATCAGAG 3420
CAGCCGATTG TCTGTTGTGC CCAGTCATAG CCGAATAGCC TCTCCACCCA AGCGGCCGGA 3480
GAACCTGCGT GCAATCCATC TTGTTCAATC ATGCGAAACG ATCCTCATCC TGTCTCTTGA 3540
TCAGATCTTG ATCCCCTGCG CCATCAGATC CTTGGCGGCA AGAAAGCCAT CCAGTTTACT 3600
TTGCAGGGCT TCCCAACCTT ACCAGAGGGC GCCCCAGCTG GCAATTCCGG TTCGCTTGCT 3660
GTCCATAAAA CCGCCCAGTC TAGCTATCGC CATGTAAGCC CACTGCAAGC TACCTGCTTT 3720
CTCTTGCGC TTGCGTTTTC CCTTGTCCAG ATAGCCAGT AGCTGACATT CATCCGGGT 3780
CAGCACCGTT TCTGCGGACT GGCTTCTAC GTGTTCCGCT TCCTTAGCA GCCCTGCGC 3840
CCTGAGTGCT TGCAGGAGCG TGAAGCTAA AAAACTGCAA AAAATAGTTT GACTTGTGAG 3900
CGGATAACAA TTAAGATGTA CCCAATTGTG AGCGGATAAC AATTCACAC ATTAAAGAGG 3960
AGAAATTACA TATG 3974

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 112 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAGCTAAAAA AACTGCAAAA AATAGTTGA CTTGTGAGCG GATAACAATT AAGATGTACC	60
CAATTGTGAG CGGATAACAA TTTCACACAT TAAAGAGGGAG AAATTACATA TG	112

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AAAAATACAG TGGCTTTATT TCCATTGTTT ATAGTCCCCA GTATCCCATC TGATAAGAAC	60
CTTCAATTCT ATAAACAAAA ATATTCAGG AAAGTATGTT ACACAATAGT ACATATAAGT	120
AATAGTTGG CAGAATTTTA AACTCTAGTA GTTCATACCC CCAAAAAACA AATTTAAAN	180
TTCAAAAAATA ACAGTTTAT TTAACATATG TTACACCTTA ACATTTAAA TATCATGCTC	240
TAGTTAAATA TTTCATCAAC AACACTGTAT ACANNTAAA TATTACATAA AATATATT	299

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 282 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TTTTGCCAGA AGGCAAGCAA TCCGGGAATC CTGGGGCCAA GAAAGCAACG CAGGGAACCA	60
AACGGTGGTG CGAGTNTTCC TGCTGGGCCA GACACCCCA GAGGACAACC ACCCCGACCT	120
TTCAGATATG CTGAAATTG AGAGTGAGAA GCACCAAGAC ATTCTTATGT GGAACTACAG	180
AGACACTTTN TTCAACTTGT CTCTGAAGGA AGTGCTGTTT CTNAGGTGGG TAAAGTACTTC	240
CTGCCAGAC ACTGAGTTG TTTCAAGGG CGATGACGAT GT	282

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TTTGCCAGA AGGCAAGCAA TCCGGGAATC CTGGGGCCAA GAAAGCAACG CAGGGAACCA	60
AACGGTGGTG CGAGTNTTCC TGCTGGCCA GACACCCCCA GAGGACAACC ACCCCGACCT	120
TTCAGATATG CTGAAATTTG AGAGTNAGAA GCACCAAGAC ATTCTTATGT GGAACCTACAG	180
AGACACTTTC TTCAACTTGT CTCTGAAGGA AGTGCTGTTT CTCAGGTGGG TAAGTACTTC	240
CTGCCAGAC ACTGAGTTG TTTCA	266

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTTGCAAAAT GAGAACATG GTGTGACACT CATCTAATTG ATCTTGTGTT GATGTTATGG	60
TCATAATAAG GAGAAANAGG GTTTAATTTC NCTTGTATTT GGTTTCCTGG TGGTATCATA	120
GTGTAATTTC AGTATTGAA AATCAGTGTG ATTCCTTAAT GGCCAACTGA AGATTGAATT	180
GCCGCTAACCA ACCATATCGT GTTAGTGAAT TTNCATATG GACCAGGAAG GCATATGTAT	240
TTTGAACTCG GAGTGAAAAG GTTGGAAAGTT ACAGACTTTT TGGCATAGGT GGGTTGGTC	300
CAATTTAAA ATTCCCGAAT TTATTNNNTG NCNNNTNTN CACATGGGNG GTTATTACAG	360
G	361

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TTGTTGGGTA TCCTGATGAT GGCAAATGTC TTCATTATT TTATTATGGA AGTCTCCAAA	60
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AGCAGTAGCC AAGAAAAAAA TGGAAAAGGG GAAGTAATAA TACCCAAAGA GAAGTTCTGG	120
AAGATATCTA CCCCTCCCGA GGCATACTNG AACCGAGAGC AAGAGAAGCT GAACCAGCAG	180
TACAACCCCA TCCTGAGCAT GCTGACCAAC CAGACGGGG AGGCAGGCAG GCTCTCCAAT	240
ATAAGNCATC TGAACACT	259

(2) INFORMATION FOR SEQ ID NO:15:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 195 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

AAAAAATACAG TGGCTTTATT TCCATTGTTT ATAGTCCCCA GTATCCCATC TGATAAGAAC	60
CTNCAATTCT ATAAACAAAA ATATTCAAG AAAGTATGTT ACACAAATAGT ACATATAAGT	120
AATAGTTGG CAGAATTTA AACTCTAGTA GTTCATACCC CCAAAAAACA AATTTAAAAA	180
TTCAAAAATA ACAGT	195

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 521 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CTATAATATT CCTACTTCCC ATAATAATGA CTGATTATT TGTAATTCAG GTATTATCAA	60
ACCTATTGGC TACAAAGACT TTGTTAAACA TTATCCAGTG GTTTCGTGA AATGGAATTA	120
TGTTTATTT TATGGGATTT GGGTAAATT TAAATTGTCT AGAAAATGTA AATTCAGTT	180
GTCAGTTGTG GAATTCAAGTT TTTCAATTGT GGAAATTCC TGCCACCCCA ACAGTATTT	240
TGTGTGTTAA TTAATTTCG AAAATGAGAA TCATGGTGTG ACACTCATCT AATTTATCTT	300
GTTGTGATGT TATGGTCATA ATACGGAGAA AGAGGGTTA ATTTTCTTG TATTTGGTT	360
CCTGGTGGTA TCATAGTGTAA ATTTAGTAT TTGAAAATCA GTGTGATTCC TTAATGGCCA	420
ACTGAAGATT GAATTGCCGC TAACAACCAT ATCGTGTAG TGAATTTCA ATATGGACCA	480

GGAAGGCATA TGTAAATTGAGCTTGAGTGA AAAGGTTGAA G 521

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

AATAGATACA AACTCAATTGAGCTTGAGTGA AAAGGTTGAA G	521
TCTCACATTA GAGTAATTGAGCTTGAGTGA AAAGGTTGAA G	60
ATTTGAGGGC CTCTAAACCC TTCAATTGAGCTTGAGTGA AAAGGTTGAA G	120
GTAATTGAGGGC CTCTAAACCC TTCAATTGAGCTTGAGTGA AAAGGTTGAA G	180
TCATTTTAA AAAACTTGTA CCCTCTTATC TGAAATCCTG TTTCTGGAAT TTGGCCATT	240
TAAGTGATTT TGTTTGCCT CTTCTATAAT ATTCTACTT CCCATAATAA TGACTGATTT	300
ATTTGTAATT CAGGTATTAA TAAACCTATT GGCTACAAAG ACTTTGTTAA ACATTATCCA	360
GTGGTTTCG TGAAATGGAA TTATGTATAT TTTTATGGGA TTTGGGAAAT TTTAAATTGT	420
CTAGAAAATGAAATTCAG TTGTCAGTTG TGGAATT	480
	517

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 462 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

ATACTGTTGG GGTGGCAGGA AATTCCACA ATTGAAAAAC TGAATTCCAC AACTGACAAC	60
TGAAATTCA GTTTCTAGA CAATTAAAAA TTTACCCAAA TCCCATAAAA ATAAACATAA	120
TTCCATTTCA CGAAAACCAC TGGATAATGT TTAACAAAGT CTTTGTAGCC AATAGGTTA	180
TAAATACCTG AATTACAAAT AAATCAGTCA TTATTATGGG AAGTAGGAAT ATTATAGAAG	240
AGGGCAAACA AAATCACTTA AAATGCCAA ATTCCAGAAA CAGGATTCA GATAAGAGGG	300
TACAAGTTT TTAAAAATNG ACCACTAGCC GGTAAGATCA GAACCAATCA TCCTGCCATA	360

TCATCCGTA AAAAAAATTA CCATCTTCCG CTTTCCCTCT TCACGTGAGT ACCAAATTGG	420
AAGGGGTTAG AGGCCCTCAA ACGGGTATCA CTCATAAAGG CA	462

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CTNTAATTAA CACACAAAAA TACTGTTGGG GTGGCAGGAA ATTTCCACAA TTGAAAAACT	60
GAATTCCACA ACTGACAAC TAAACATAAT TCCATTCAC GAAAACCACT GGATAATGTT TAACAAAGTC	120
TTTGTAGCCA ATAGGTTTAT AAATACCTGA ATTACAAATA AATCAGTCAT TATTATGGGA	180
AGTAGGAATA TTATNGAAGA GGGCAAACAA AATCACTTAA AATGGCCAAA TTCCAGAAC	240
AGGATTTCAAG ATAAGAGGGT ACAAGTTTT TAAAAATGAC CACTAGCCGG TAAGATCAGA	300
ACCAATCATC CTGCCATATC ATCCGTAAAA NAAAATTACC ATCTTCCGCT TTCCCTCTTC	360
ACGTGAGTAC CAAATTGAAG GGTTTAGG	420
	448

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 857 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

NGNGGTNNCG TCGGTTAAAT ATTCAAGACC AAAGCCAAAG ATCTCTTCAT AGGTGATGTG	60
ATCCACAATG CTGGACCTCA TCGGGATAAG AAGCTGAAGT ACTACATCCC AGAAGTTGTT	120
TACTCTGGCC TCTACCCACC CTATGCAGGG GGAGGGGGGT TCCTCTACTC CGGCCACCTG	180
GCCCTGAGGC TGTACCATAT CACTGACCAAG GTCCATCTCT ACCCCATTGA TGACGTTTAT	240
ACTGGAATGT GCCTTCAGAA ACTCGGCCTC GTTCCAGAGA AACACAAAGG CTTCAGGACA	300
TTTGATATCG AGGAGAAAAA CAAAAATAAC ATCTGCTCCT ATGTAGATCT GATGTTAGGA	360

CATAGNAGGA	AAACCTCAAG	AGATGATTGA	TATTTGGGCT	CAAGNTGCAG	AGTGCTCAAT	420
TTAAAATGCT	AAAATAGATA	CAAACCTCAAT	TTGGGATTNG	AAGGGGTTTT	TNGGATTGGC	480
CCCATNTGGG	GTCTTNANAT	TAGAGNNGGT	TCAAGTGGGT	ACAGTGATGA	AAANNNNNN	540
NNNNGGNNNN	NNNNCCNNNT	NNTTNNAANN	NNNNNNNNNN	NNNNNNNNNN	NNTNNCANN	600
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	660
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	720
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	780
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	840
NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	NNNNNNNNNN	857

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GAGATGATTG	ATATTTGGTC	TCAGTTGCAG	AGTGCTCATT	TAAAATGCTA	AAATAGATAC	60
AAACTCAATT	TTGCATAGAA	AGGTGTATTT	TGAATAGTTC	CCATGTTGTG	TTCTCACATT	120
AGAGTAATTT	CTGTATTAAA	CCATGAAAAT	TGCCTTTATG	AGTGATACCC	ATTTGAGGGC	180
CTCTAAACCC	TTCAATTGG	TACTCACGTG	AAGAGGGAAA	GCGGAAGATG	GTAATTTTT	240
TTTACGGATG	ATATGGCAGG	ATGATTGGTT	CTGATCTTAC	CGGCTAGTGG	TCATTTTAA	300
AAAACTTGTA	CCCTCTTATC	TGAAATCCTG	TTTCTGGGAA	TTTGGCCATT	TTAAGTGATT	360
TTGTTTGCCC	TCTTCTATNA	ATATCCTAC	TTCCCNATAAT	AATGACTGAT	TTNATTGTA	420
ANTCAGGNAT	TTATNAAACC	CTTGGGCTAC	CAAGNCTTGT	TAAACAT		467

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 442 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TACTGTTGGG	GTGGCAGGAA	ATTTCCAAAA	TTGAAAAACT	GAATTCCACA	ACTGACAAC	60
GAAATTCAG	TTTCTAGAC	AATTAAAAT	TTACCCAAAT	CCCATAAAAA	TAAACATAAT	120
TCCATTCAC	GAAAACCACT	GGATAATGTT	TAACAAAGTC	TTTAGTAGCCA	ATAGGTTTAT	180
AAATACCTGA	ATTACAAATA	AATCAGTCAT	TATTATGGGA	AGTAGGAATA	TTATAGAAGA	240
GGGCAAACAA	AATCACTTAA	AATGCCAAA	TTCCAGAAC	AGGATTCAG	ATAAGAGGGT	300
ACAAGTTTT	AAAAAATGAC	CACTAGCCCG	GTAAGATCAG	AACCAATCAT	CCTGCCATAT	360
CATCCGTAAA	AAAAAATTAC	CATCTTCCGC	TTTCCCTCTT	CACGTGAGTA	CCAAATTGGA	420
AGGGGTTAGA	GGCCCNCCAA	CG				442

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 575 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

TACTGTTGGG	GTCGGCAGGA	AATTCCACA	ATTGAAAAAC	TGAATTCCAC	AACTGACAAC	60
TGAAATTCAG	TTTCTAGA	CAATTAAAA	TTTACCCAA	TCCCATAAAA	ATAAACATAA	120
TTCCATTCAG	CGAAAACAC	TGGATAATGT	TTAACAAAGT	CTTGTAGCC	ATAGGTTA	180
TAAATACCTG	AATTACAAAT	AAATCAGTC	TTATTATGGG	AAGTAGGAAT	ATTATACGAA	240
GAGGGCAAAC	AAAATCACTT	AAAATGCCA	AATTCCAGAA	ACAGGATTTC	AGATAAGAGG	300
GTACAAGTTT	TTTAAAAATG	ACCACTAGCC	CGGTAAAGATC	AGAACCAATC	ATCCCTGGCC	360
ATATCATCCG	GTAAAAAAA	ATTACCATCT	TCCGCTTTTC	CCTCTTCACG	TGAGGTACCC	420
AATTGGAANG	GGTTTAGAAG	GCCCTCAAAC	GGGTATCACT	CNTTAAAGGC	ANTTCATGG	480
GTAAATATGG	AATTACCNCT	AATGGTGAGA	CCCCACCTGG	GGACTATTCC	AAATACCCCT	540
TCCATGGCAA	ATTGGNGTTG	GAACCANTTT	AGCAT			575

(2) INFORMATION FOR SEQ ID NO:24:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 511 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GGATACCCAT TTGAGGGCCT CAAACCCCTT CAATTTGGTA CTCACGTGAA GAGGGAAAGC	60
GGAAGATGGT AATTTTTTTT TATGGATGAT ATGGCAGGAT GATTGGTTCT GATCTTACCG	120
GCTAGTGGTC ATTTTAAAAA AACTTGTACC CTCTTATCTG AAATCCTGTT TCTGGAATTT	180
GGCCATTTA AGTGATTTG TTTGCCCTCT TCTATAATAT TCCTACTTCC CATAATAATG	240
ACTGATTTAT TTGTAATTCA GGTATTTATA AACCTATTGG CTACAAAGAC TTTGTTAAC	300
ATTATCCAGT GGTTTTCGTG AAATGGGAAT TATGTTATT TTTATGGGA TTTGGGTAAA	360
TTTAAATTG TCTAGGAAAA CTGAAATTCT CAGTTGTCCA GTTGTGGAA TTCAGTTTT	420
CCAATTGTGG GAAATTCCC GGCCACCCCA ACAGTATTCT TGTGTGGTTA ATTAATTCTT	480
GCCAAATGAG GATCCNGGGT GTGACCACTN T	511

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 400 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

GTAAATTTA AATTGTCTAG AAAACTGAAA TTTCAGTTGT CAGTTGTGGA ATTCA	60
TCAATTGTGG AAATTCCTG CCACCCCAAC AGTATTTTG TGTGTTAATT AATTTGCAA	120
AATGAGAACATC ATGGTGTGAC ACTCATCTAA TTTATCTTGT TGTGATGTTA TGGTCATAAT	180
AAGGAGAAAG AGGGTTAAT TTTCTTGTAA TTTGGTTCC TGGTGGTATC ATAGTGTAAAT	240
TTTAGTATTT GAAAATCAGT GTGATTCTT AATGGGCCAA CTGAAGATTG AATTGCCGCT	300
AACAACCATA TCGTGTAGT GAATTTCAA TATGGGACCN GGAAGGGCAT ATGTATTTG	360
GAACTTGGAG TGGAAAAGGT TGGAGTTACA GACTTTGGC	400

(2) INFORMATION FOR SEQ ID NO:26:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 480 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

TGAGGGTCAC	GTCGGTGGTT	ACGGGTTTA	ACAACCTGCC	GGACAGATT	AAAGACTT	60
TGCTGTATT	GAGATGCCGC	AATTATTAC	TGCTTATAGA	TCAGCCGGAT	AAGTGTGCAA	120
AGAAACCTTT	CTTGTGCTG	GCGATTAAGT	CCCTCACTCC	ACATTTGCC	AGAAGGCAAG	180
GCAATCCGGG	AATCCTGGGG	CCAAGAAAGC	AACGCAGGGA	ACCAAACGGT	GGTGCAGTC	240
TTCCTGCTGG	GCCAGACACC	CCCAGAGGAC	AACCACCCCG	ACCTTCAGA	TATGCTGAAA	300
TTTGAGAGT	GAGAAGCACC	AAGACATTCT	TATGTGGAA	CTACAGAGGA	CACTTCCTT	360
CAANTGTCT	NTGGAAGGAA	GTGCTTTT	TTCAGGTGGG	GTAAAGTTAT	TTCCTGCCA	420
GACATTGAGT	TTGTTTTTC	AAGGGCGAT	GGACGATGTT	TTTGTGNAC	ACCCTTCACT	480

(2) INFORMATION FOR SEQ ID NO:27:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TTAATTAACA	CACAAAAATA	CTGTTGGTA	NANNAANAAA	TTTCCACAAT	TGAAAAACTG	60
AATTCCACAA	CTGACAAC	AAATTCAGT	TTCTAGACA	ATTTAAAATT	TACCAAATC	120
CCATAAAAAT	AAACATAATT	CCATTCACG	AAAACCACTG	GATAATGTTT	AACAAAGTCT	180
TTGTAGCCAA	TAGTTTATA	AATACCTGAN	TTACAAATAA	ATCAGTCATT	ATTATGGAA	240
GTAGGAATAT	TATAGAAGAG	GGCAAACAAA	NTCACTAAA	ATGCCAAAT	TCCAGGANAC	300
AGGGATTCA	GATAAGAGGG	TACAAGTNTT	TTAAAAGTGA	CCACTAGGCC	GGTAAGGTC	360
CGGANCCAAT	CATCCTGCCA	TNTTCATCCG	TA			392

(2) INFORMATION FOR SEQ ID NO:28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

GNCCCCAGTA TCCCACATCTGA TAAGAACCTT CAATTCTATA AACAAAAATA TTTCAAGAAA	60
GTATGTTACA CAATAGTACA TATAAGTAAT AGTTTGGCAG AATTTTAAAC TCTAGTAGTT	120
CATACCCCCA AAAAACAAAT TTTAAAATTC AAAAATAACA GTTTTATTAA ACATATGTTA	180
CACCTTAACA TTTAAAATAT CATGCTCTAG TTAAATATTT CATCAACAAAC ACTGTATACA	240
ANTAAAATAT TACATAANAT ATATTTAAGG NAAATGTTT GGGTCTTGA TCTGGAACAN	300
TAAATAAAAA CACGGGCACT TCTACATAGG ACGGGGGTGG CGGTTACTAC TCCAATAATA	360
ATCNTGGTNT AGGGCGGCCT G	381

(2) INFORMATION FOR SEQ ID NO:29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 323 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GATCAAAGAC CAAAACATT TCTTAAATAT ATTTTATGTA ATATTTATT TGTATACAGT	60
GTTGTTGATG AAATATTTAA CTAGAGCATG ATATTTAAA TGTTAAGGTG TAACATATGT	120
TAAATAAAAC TGTTATTTN GAATTNAAA ATTNGTTT NGGGGGTATG ANCTACTAGA	180
GTTTAAAATT CTGCCAAACT ATTACTTATA TGTNCTATTG TGTAACATAC TTNCTNGAAA	240
TATTTNGGTT TATAGAATTG ANGGTTCTTA TCAGATGGGA TACTGGGGAC TATAAACAAAT	300
GGAAATAAAAG CCACTGTATT TNT	323

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

AAAAATACAG TGGCTTTATT TCCATTGTTT ATAGTCCCCA GTATCCCATC TGATAAGAAC	60
CTTCAATTCT ATAAACAAAA ATATTTCAAG AAAGTATGTT ACACAAATAGT ACATATAAGT	120

AATAGTTGG CAGAATTAA AACTCTAGTA GTTCATACCC CCAAAAACA AATTTAAAN	180
TTCAAAAATA ACAGTTTAT TTAACATATG TTACACCTTA ACATTTAAAAT TATCATGCTC	240
TAGTTAAATA TTTCATCAAC AACACTGTAT ACANNTAAAAT TATTACATAA AATATATT	299

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

GACAGATTAA AAGACTTTCT GCTGTATTTG AGATGCCGCA ATTATTCACT GCTTATAGAT	60
CAGCCGGATA AGTGTGCAAA GAAACCTTTC TTGTTGCTGG CGATTAAGTC CCTCACTCCA	120
CATTTGCCA GAAGGCAAGC AATCCGGAA TCCTGGGCC AAGAAAGCAA CGCAGGGAAC	180
CAAACGGTGG TGCGAGTCCTT CCTGCTGGC CAGACACCCC CAGAGGACAA CCACCCGAC	240
CTTTCAGATA TGCTGAAATT TGAGAGTTAG AAGCACCAAG ACATTCCTTA TGTGGGACCT	300
ACA	303

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 317 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTTATTTCCA TTGTTTATAG TCCCCAGTAT CCCATCTGAT AAGAACCTTC AATTCTATAA	60
ACAAAAAATAT TTCAAGAAAG TATGTTACAC AATAGTACAT ATAAGTAATA GTTGGCAGA	120
ATTTTAAACT CTAGTAGTTC ATACCCCCAA AAAACAAATT TTAAAATTCA AAAATAACAG	180
TTTTATTTAA CATATGTTAC ACCTTAACAT TTAAAATATC ATGCTCTAGT TAAATATTTC	240
ATCAACAAACA CTGTATACAA ATAAAATATT ACATAAANTAA TATTTAAGGN AAATGTTTG	300
GGTCTTTGAT CTGGAAC	317

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 325 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

TTAAAAATAN AGTGGCTTA TTTCCATTGT TTATAGTCCC CAGTATCCCA TCTGATAAGA	60
ACCTTCAATT CTATAAACAA AAATATTCA AGAAAGTATG TTACACAATA GTACATATAA	120
GTAATAGTTT GGCAGAATT TAAACTCTAG TAGTTCATAC CCCCCAAAAAA CAAATTTAA	180
AATTCAAAAAA TAACAGTTTT ATTTAACATA TGTTACACCT TAACATTTAA AATATCATGC	240
TCTAGGTTAA ATATTCATC AACAAACACTG GTATACAAAT AAAATATTAC ATAAAATATA	300
TTTAAGGGAA ATGTTTGGG GCTTT	325

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 282 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

TTTGCCAGA AGGCAAGCAA TCCGGGAATC CTGGGGCCAA GAAAGCAACG CAGGGAACCA	60
AACGGTGGTG CGAGTNTTCC TGCTGGCCA GACACCCCCA GAGGACAACC ACCCCGACCT	120
TTCAGATATG CTGAAATTG AGAGTGAGAA GCACCAAGAC ATTCTTATGT GGAACTACAG	180
AGACACTTTN TTCAACTTGT CTCTGAAGGA AGTGCTGTTT CTNAGGTGGG TAAGTACTTC	240
CTGCCAGAC ACTGAGTTG TTTCAAGGG CGATGACGAT GT	282

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 358 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: both
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

AATTCACAC	ATTGAAAAAC	TGAATTCCAC	AACTGACAAC	TGAAATTCA	GTTTCTAGA	60
CAATTAAAA	TTTACCCAAA	TCCCATAAAA	ATAAACATAA	TTCCATTCA	CGAAAACCAC	120
TGGATAATGT	TTAACAAAGT	CTTTGTAGCC	AATAGGTTA	TAAATACCTG	AATTACAAAT	180
AAATCAGTCA	TTATTATGGG	AAGTAGGAAT	ATTATAGAAG	AGGGCAAACA	AAATCACTTA	240
AAATGCCAA	ATTCCAGGAA	ACAGGGATT	CAGGATAAGG	GGGTACAAGT	TTTTAAAAAA	300
TGGACCACTA	GGCCGGGTAA	GGATCAGGAA	CCANTTCATC	CTGGCCATAT	TCATCCGT	358

(2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 428 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

ACTTCCTGCC	CAGACACTGA	GTGGTTTC	AAGGGCGATG	ACGATGTTT	TGTGAACACC	60
CATCACATCC	TGAATTACTT	GAATAGTTA	TCCAAGACCA	AAGCCAAAGA	TCTCTTCATA	120
GGTGATGTGA	TCCACAATGC	TGGACCTCAT	CGGGATAAGA	AGCTGAAGTA	CTACATCCCA	180
GAAGTTGTTT	ACTCTGGCCT	CTACCCACCC	TATGCAGGGG	GAGGGGGGTT	CCTCTACTCC	240
GGCCACCTGG	GCCTGAGGCT	GTACCATATT	CACTGGACCA	GGGTCCATCT	CTTACCCCAT	300
TGGATGGACG	TTTTATACTG	GGAATGTGNC	CTTCAGGAAA	NTCGGGCCTC	GTTTCCAGGA	360
GGAAACACAA	AGGGTTTCAG	GGGACATT	GATATTGAG	GGGAGGGAAA	AACAAAAANT	420
TAACATTT						428

(2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

TTTGCCAGA	AGGCAAGCAA	TCCGGGAATC	CTGGGGCCAA	GAAAGCAACG	CAGGGAACCA	60
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AACGGTGGTG CGAGTNTTCC TGCTGGCCA GACACCCCCA GAGGACAACC ACCCGACCT	120
TTCAGATATG CTGAAATTG AGAGTNAGAA GCACCAAGAC ATTCTTATGT GGAACATACAG	180
AGACACTTTC TTCAACTTGT CTCTGAAGGA AGTGCTGTT CTCAGGTGGG TAAGTACTTC	240
CTGCCAGAC ACTGAGTTG TTTCA	266

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 259 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTGTTGGGTA TCCTGATGAT GGCAAATGTC TTCATTATT TTATTATGGA AGTCTCCAAA	60
AGCAGTAGCC AAGAAAAAAA TGGAAAAGGG GAAGTAATAA TACCCAAAGA GAAGTTCTGG	120
AAGATATCTA CCCCTCCCGA GGCATACTNG AACCGAGAGC AAGAGAAGCT GAACCGGCAG	180
TACAACCCA TCCTGAGCAT GCTGACCAAC CAGACGGGGG AGGCGGGCAG GCTCTCCAAT	240
ATAAGNCATC TGAACTACT	259

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 247 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TTATAGNCCC CAGTATCCC TCTGATAAGA ACCTTCAATT CTATAAACAA AAATATTCA	60
AGAAAGTATG TTACACAATA GTACATATAA GNAATAGTTT GGCAGAAATT TAAACTCTAG	120
TAGTTCATAC CCCCAAAAAA CAAATTTAA AATTCAAAAA TAACAGTTT ATTAAACATA	180
TGTTACACCT TAACATTTAA AATATCATGC TCTNGTTAAA TATTCATCA ACAACACTGT	240
ATACAAA	247

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 368 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

CTGATGTTAG TACATAGTAG AAAACCTCAA GAGATGATTG ATATTTGGTC TCAGTTGCAG	60
AGTGCTCATT TAAAATGCTA AAATAGATAAC AAACCTCAATT TTGCATAGAA AGGTGTATTT	120
TGAATAGTTC CCATGTTGTG TTCTCACATT AGAGTAATTT CTGTATTAAA CCATGAAAAT	180
TGCCTTATG AGTGATACCC ATTTGAGGGG CCTCTTAAAC CCTTCAATTG GGGTACTTCA	240
CGTGAAGAGG GGAAAGCGGG AAGATGGTA ATTTTTTTT ACGGGATGGA TATGGGCNGG	300
GATGATTGGG TTCTGGATCC TTACCCGGCC TAGTGGGTCC ATTTTTAAA AAACTTGGTA	360
CCCCCNCC	368

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

AAAAATACAG TGGCTTTATT TCCATTGTTT ATAGTCCCCA GTATCCCATC TGATAAGAAC	60
CTNCAATTCT ATAAACAAAA ATATTTCAAG AAAGTATGTT ACACAATAGT ACATATAAGT	120
AATAGTTGG CAGAATTTA AACTCTAGTA GTTCATACCC CCAAAAAACA AATTTAAAAA	180
TTCAAAAATA ACAGT	195

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 2257 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: both
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

GAAATATTT TGTTTATAGA ATTGAAGGTT CTTATCAGAT GGGATACTGG GGACTATAAA 60
CAATGGAAAT AAAGCCACTG TATTTTAAT TTTTGTGTA ATGTGTAATC TATAATCCTT 120
TTGTTTCCCA TATTTGAGAA CATTTCCTCC TGAAAGAGGC CAGTTCCCTC CCCAGAAACC 180
ATTACAGTAG TGTTGAACTA TCACTGTCTC TCAGTGCCTC ATCCATCTT GCATTTAAAA 240
TCCCCAAAGT GCTTCCCAT TTAAAGTCTT TAAAGAAAAG TGAGAATATT TATTTATGCT 300
TCCATTTCA GTGAGTATAA ATAATTAAAT TAGGGAGTGG TGTGGCATTG TAAAGATTGT 360
GTTATCCTAA GCCATTCTA TTTGGAGTT TGTAGCCACA AAGATGAAAT ATAGAATCAG 420
CCTTGACTAC TCAATTCCCT TTCATAGACC CATGTTGAGA AGACACTACT AACGTCCAGT 480
GGGAAACAAG TAGACAATTG ATGAAGCTCA AAAAACAGAA GGTTAGTGT TGTAAGAGCA 540
AACAGTCTAA TCCTGTTGG AATGTGGAAG CCATTCTGA GCAAGTATGA GGACACAGGT 600
GCTTGATTG AGATTGAAGA CTGTTTCAG CCTGGTCTTC CTGAAGGTTT CCTGGGCCT 660
GCATCTGCCT TCTACTCCCA TGGCTGCTAG CACACACCTC CCAGAGGGCC ATATTGCCAC 720
ATTATGGCTA GAGAAGAGTA AAGAAGAAA GAAGCTCTGA GAACATTACAGTAATTGG 780
ATCACATTG CATTGTCCA AAAACCTGA CCACGCATTC TCAGGTAATA GGTTCTCCT 840
CTCAGAGGAA TTTCAATTG TTTCTTGTT AGAGATTCCC CTTCTCTGAG GTTCAAGTC 900
TCTTGTAGAG AAAGAAGAGA TGGAGCAGGT TTTGAATGAG GTGTGGAGGG CCACTGGGG 960
GCCTTTGTG AGCCTTCAGT CCACATGTGT GCTGTTGTT GAACATGAGT TCTTGGTGCT 1020
GATGACATTG GGATGAGATG ATCTCTGGCC CTTCTTCATT TGGCAGAAGT TCTTGTGCAA 1080
TGGCTGCCCA AGCCCACAC ACTGGTCATT GCTGCCCTGT GAGATGGACC TCATGGCCTT 1140
TTTAGCAGAG CACGTTAGGT TTTAGAGCTT TACGCATGCT TGGGCTCTGT TATGGCGCAA 1200
ACCCTTAAAT CCAGGAAGGC CTCTCTGGT GCCCACAATA TGGGTTCTCA CCTGATCCCC 1260
CATCTCACGG ATGGAACTGC TGTAAGTCTA ACTTATTCTT TGAGAACTGT TTAACAATTA 1320
GGCCTCAAGG GAAACTGGTA TTTGGGCCCT TTTCTTGCT TATTCCAAG TCATGTTGAT 1380
TTTGAGTTG AAGGTCAAAA AGGCTGAAAG CATTGCCAGG GTTGGACTA TTCAAAAACC 1440
CAAGCAGGTC TTAAAAAAAG GATGCAAGAG ACAAGAATGG CTCATTCCCC TTCCCTGATCC 1500
TGGTTATACC CATGTCCTT CTTGAGATGG TCAAGAGAGG CTGAAAGAA GAACAGGAAA 1560
TTGGGGAGT GCTTGTAC ACTTGGAAAT TGAGTCAAGA ATTAAAGACA CCCAAAGTGG 1620
GCCATCTCCT ACTTGTCCAC ACCTGATTGG TGGTGTGCG GAATATTGA TGTCCCGGGT 1680
CATCTTGACT TTCTCAGATG CAAAAAGGGAA GGGTGACTTT ACTAATGGAA AGGATGGAA 1740
GCTGAAATGA ATGAAGCCTT CAGTTGGGCC AAAGTTAAC TTCCCCGTGA TTTGCCTTCT 1800
GATGAAAAAT GCCAGATGAA GTGAAAATTC TTGTTCTTG CCTAGAACAG GAAAATACAT 1860

ACTTTACATG CTGGGCTATT GAGGCTATGA AATTAGGTTT TCCTTAATGT AAATCCAATT	1920
GCTAGAAACA TTTGCCAAAT AAGATTTTT GAACTGAACT TTGTTGCAT TAATCTGAAA	1980
AACTGAAGTA TTCTGACTCA TGAAGTTCTC AAAGTAATAC ACTAAAAAAG TTTTGCCTT	2040
AATACCATTA TATCTTGTAG AGGCCAAGAA TGAGGGACTT CTGTCTTAA AGAGCCCTAA	2100
AAATCTCGTT TGCTCACATG ATATGAATTA CCGTATTTGT TGTAAATGCG CAACTTGTA	2160
TACACTAAAA GCACTGCCAA TATGATTTT TATCAGTTGT GCCTCAGTTA GAGATATTAA	2220
AATGTGACAT CTTAAATATT ACATATTAGA ATAATTG	2257